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FIG. 1A

1 CGGACGCGTGGGCGCGCAGCCTGGCTGACCTGATCCTGGACCAGTGCCCCGACCGCGGCG 60

61 CGCCGGTGCCGCGAGATGCTGGCCCAGCCGCGAGCGGCTGCTCTTCATCCTGGACGGCGCGG 120
1 M Q A Q P Q R L Q F I L D G A D 16

121 ACGAGCTGCCGGCGCTGGGGGGCCCCGAGGCCGCGCCCTGCACAGACCCCTTCGAGGCGG 180
17 E L P A L G G P E A A P C T D P F E A A 36

181 CGAGCGGCGCGGGTGCTAGGCGGGCTGCTGAGTAAGGCGCTGCTGCCACGGCCCTCC 240
37 S G A R V Q G G Q Q S K A L Q P T A L L 56

241 TGCTGGTGACCACGCGCGCCGCCCGGGAGGCTGCAGGGCCGCTGTGTCCCCGC 300
57 Q V T T R A A A P G R Q Q G R L C S P Q 76

301 AGTGCGCCGAGGTGCGCGGCTTCTCCGACAAGGACAAGAAGAAGTATTTCTACAAGTTCT 360
77 C A E V R G F S D K D K K K Y F Y K F F 96

361 TCCGGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCGTGAAGGAGAACGAGACGCTGT 420
97 R D E R R A E R A Y R F V K E N E T Q F 116

421 TCGCGCTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTGTGCACCGTGCTGCGCCAGCAGC 480
117 A Q C F V P F V C W I V C T V Q R Q Q L 136

481 TGGAGCTCGGTCCGGACCTGTGCGGCACGTCCAAGACCACCGTCAGTGCTACCTGCTTT 540
137 E L G R D L S R T S K T T T S V Y Q L F 156

541 TCATCACCAGCGTTCTGAGCTCGGCTCCGGTAGCCGACGGGCCCCGGTTGCAGGGCGACC 600
157 I T S V L S S A P V A D G P R L Q G D Q 176

601 TGCGCAATCTGTGCCGCTGGCCCCGAGGGCGTCCTCGGACGCAGGGCGCAGTTTGCCG 660
177 R N Q C R Q A R E G V L G R R A Q F A E 196

661 AGAAGGAAC TGAGCAACTGGAGCTTCGTGGCTCCAAAGTGACAGACGCTGTTTCTCAGCA 720
197 K E Q E Q L E L R G S K V Q T L F L S K 216

721 AAAAGGAGCTGCCGGGCGTGCTGGAGACAGAGGTCACCTACCAGTTCATCGACCAGAGCT 780
217 K E L P G V L E T E V T Y Q F I D Q S F 236

781 TCCAGGAGTTCCTCGCGGCACTGTCTACCTGCTGGAGGACGGCGGGGTGCCAGGACCG 840
237 Q E F L A A L S Y L Q E D G G V P R T A 256

841 CGGCTGGCGGCGTTGGGACACTCCTGCGTGGGGACGCCAGCCGCACAGCCACTTGGTG 900
257 A G G V G T L Q R G D A Q P H S H L V L 276



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FIG. 1B

901	TCACCACGCGCTTCCTCTTCGGACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCC	960
277	T T R F L F G <u>L</u> S A E R M R D I E R H	296
961	ACTTCGGCTGCATGGTTTCAGAGCGTGTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGGAC	1020
297	F G <u>C</u> M V S E R V K Q E A L R W V Q G Q	316
1021	AGGGACAGGGCTGCCCCGAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTCGAGG	1080
317	G Q G C P G V A P E V T E G A K G L E D	336
1081	ACACCGAAGAGCCAGAGGAGGAGGAGGAGGAGGCCCAACTACCCACTGGAGTTGC	1140
337	T E E P E E E E E G E E P N Y P L E L <u>L</u>	356
1141	TGTACTGCCTGTACGAGACGCAGGAGGACGCGTTTGTGCGCCAAGCCCTGTGCCGGTTCC	1200
357	Y <u>C</u> <u>L</u> Y E T Q E D A F V R Q A L C R F P	376
1201	CGGAGCTGGCGCTGCAGCGAGTGCCTTCTGCCGCATGGACGTGGCTGTTCTGAGCTACT	1260
377	E L A L Q R V R F C R M D V A V L S Y <u>C</u>	396
1261	GCGTGAGGTGCTGCCCTGCTGGACAGGCACTGCGGCTGATCAGCTGCAGATTGGTTGCTG	1320
397	V R C C P A G Q A L R <u>L</u> I S C R L V A A	416
1321	CGCAGGAGAAGAAGAAGAGCCTGGGGAAGCGGCTCCAGGCCAGCCTGGGTGGCGCA	1380
417	Q E K K K K S <u>L</u> G K R L Q A S L G G G S	436
1381	GTTCTCAAGGCACCACAAAACAAGTCCAGCCTCCCTTCTTCATCCACTCTTTCAGGCAA	1440
437	S Q G T T K Q <u>L</u> P A S L L H P L F Q A M	456
1441	TGACTGACCCACTGTGCCATCTGAGCAGCCTCACGCTGTCCCACTGCAAAGTCCCTGACG	1500
457	T D P L <u>C</u> H <u>L</u> S S L T L S H C K L P D A	476
1501	CGGTCTGCCGAGACCTTTCTGAGGCCCTGAGGGCAGCCCCGCACTGACGGAGCTGGGCC	1560
477	V C R D L S E A <u>L</u> R A A P A L T E <u>L</u> G <u>L</u>	496
1561	TCCTCCACAACAGGCTCAGTGAGGCGGGACTGCGTATGCTGAGTGAGGGCCTAGCCTGGC	1620
497	L H N R L S E A G L R M <u>L</u> S E G L A W P	516
1621	CGCAGTGCAAGGTGCAGACGGTCAGGGTACAGCTGCCTGACCCCCAGCGAGGGCTCCAGT	1680
517	Q <u>C</u> R V Q T V R V Q L P D P Q R G L Q Y	536
1681	ACCTGGTGGGTATGCTTCGGCAGAGCCCCGCCCTGACCACCTGGATCTCAGCGGTGCC	1740
537	<u>L</u> V G M <u>L</u> R Q S P A <u>L</u> T T L D <u>L</u> S G C Q	556
1741	AACTGCCCCCCCCATGGTGACCTACCTGTGTGCAGTCCTGCAGCACCAGGGATGCGGCC	1800
557	<u>L</u> P A P M V T Y <u>L</u> C A V <u>L</u> Q H Q G <u>C</u> G <u>L</u>	576

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FIG. 2A-1

		1		50
HLRRII1		(1)	-----	
caspase_recruitment_protein		(1)	MAGGAWGR L AC Y LE F FL K KE E EL K EF F Q L LLANKA H SRSSSG E TPAQPEK T SG	
cryopyrin		(1)	-MASTRCK L AR Y LE D EDV D LKKFK M H L ED Y PPQ K GCIP L PRG Q TEKADH	
Nucleotide_Binding_site		(1)	----MGFN L QAL L EQ L SQ D EL S KFK Y L L TTT S PA H ELQ K TPH K EV D KADG	
		51		100
HLRRII1		(1)	-----	
caspase_recruitment_protein		(51)	MEVAS Y LVAQ Y GE Q RAWD L ALH T WE Q MG L R S LCAQ A Q E GAGH S PSF P Y S P	
cryopyrin		(50)	VDLA T EM I DFNG E E K AWA M AV W IFAA T NR R DL Y E K AK R DE P K W CS D NARV	
Nucleotide_Binding_site		(47)	KQL V EL L THC D SY W W E MA S LQ V FE K M H R M D L SER A K D EVREA L K S ENK	
		101		150
HLRRII1		(1)	-----	
caspase_recruitment_protein		(101)	SEPHLGSPSQPTSTAVLMPWIHELPA G CTQGSERRVLRQLPDTSGRRWRE	
cryopyrin		(100)	SN-----	
Nucleotide_Binding_site		(97)	RK-----	





FIG. 2A-2

		151		200
HLRRSI1	(1)	-----		-----
caspase_recruitment_protein	(151)	ISASHLYQALPSSPDHESPSQESPNAPTSTAVLGSWGSPQP	PSIAPRQE	
cryopyrin	(102)	-----	PVIVICQEDS	
Nucleotide_Binding_site	(99)	-----	PLSLGITR-	
		201		250
HLRRSI1	(1)	-----		-----
caspase_recruitment_protein	(201)	APGTQWPLDETSGIMYTEIREREREKSEKGRPPMAA	VGTPPOAHSSLP	
cryopyrin	(111)	IIEEWGLLEYLSRSICKMKDYRKKYVRSRFQCIEDRNARLGESV		
Nucleotide_Binding_site	(107)	KERPPIVDVDEMLEREKTEAQDKDNRCRYILTKFEREMWKSWPGDSKEVQV		
		251		300
HLRRSI1	(1)	-----		-----
caspase_recruitment_protein	(251)	HHPMEPSVRESLCSTWPWKNEDEFNQFTQLLLLRPHPRSQDPLVKRSW		
cryopyrin	(161)	SLNKRYSRLRIKEHRSQQEREQELLAI GKTKTCESPV		
Nucleotide_Binding_site	(157)	MAERYKMLIPFSNPR		

FIG. 2A-3

		301			350
		(1)	-----	-----	
HLRRSI1		(301)	PDYVEENRGHIEIRDLFGPGIDIQEPRIVTLLOGAAGIGKSTLARQVKEA		
caspase_recruitment_protein		(199)	-----SPDKMELLFDPPDDEHSEPVETVVVFQGAAGIGKTIILARKMMLD		
cryopyrin		(172)	-----VLPQPFSTVTVLYGPAGLGKTTLAQKLMMLD		
Nucleotide_Binding_site					
		351		400	
		(1)	-----	-----MLA	
HLRRSI1		(351)	WCRGOLYCDRFQHFVYFSCRELAQSKVVVSLAELIGKDGATAPATRQILS		
caspase_recruitment_protein		(241)	WASGTLYQDRFDYLFYTHCREVSLVTQRSIGDLIMSCCPDPNPPIHKIVR		
cryopyrin		(202)	WAEDNLIHK-FKYAFYLSCRELSRIGPCSEAEVFRDWPELODDTPHLLA		
Nucleotide_Binding_site					
		401		450	
		(4)	OPQRLFLILDGADELP-ALGCPFAAPCTDPFAAGCARVLGGLISKALLP		
caspase_recruitment_protein		(401)	RPERLFLILDGVDEPGWVLOEPSSELCLLWSQPQPADALLGSLLGKTTLP		
cryopyrin		(291)	KPSRLFLIMDGFDELOGAEDDEHIQPLCTDWQKAERGDIILSSILIRKKLLP		
Nucleotide_Binding_site		(251)	QARKQLFWITDGFDELGAAPGALLIEDICGDWEKKKPVPVLLGSLINRVMLP		



FIG. 2A-4

HLRRII1	451		500
caspase_recruitment_protein	(53)	TALLVTTRAAAPGRLQGRLCSPQCAEVRGFSDDKKKYFYKFFRDERRA	
cryopyrin	(451)	EASLLITARTALQNLIPSEQARWVEVLGFSESSRKEYFYRYFTDERQA	
Nucleotide_Binding_site	(341)	EASLLITTRPVALEKQLQHLIDHPRHVEILGFSEAKRKEYFFKYFSDQA	
	(301)	KALLVTTRPRALRLRIIAEETPIYRVEGFLEEDKRAYFLRHFGEDEQA	
HLRRII1	501		550
caspase_recruitment_protein	(103)	ERAMREVKENETLFALCFVPVCWIVCTVLRQQQLGRDLRSTSKTTTSV	
cryopyrin	(501)	IRAFRLVKSNEELWALCVPWVSWLACTCLMQQMKRKEKILTSKTTTTL	
Nucleotide_Binding_site	(391)	RAAFSLIOENEVLFTMCFPIVCWIVCTGLKQOMESGKSLAQTSKTTTAV	
	(351)	MRAFEIMRSNAALFQLGSAPVCWIVCTTLKLQMEKGEDPVPTCLTRTGL	
HLRRII1	551		600
caspase_recruitment_protein	(153)	YLLFLTSTVLSSAPVADGPRLQGLRNLCRLAREGVLCRRQAFAEKELTQL	
cryopyrin	(551)	CLHVLAAQALQAQP-----LGPQLRDLCSLAAEGIWOKKLFSPDDLKXH	
Nucleotide_Binding_site	(441)	YVFLSSLLQPRGGSQEHGLCAHLWGLCSLAADGIMNQKILFFESDILRNH	
	(401)	ELRFLCSREP-----QGAQLRGALRTLSSLAAQGLWAQTSVLRHREDLERI	



FIG. 2B-1

HLRSI1	(203)	ELRGSKVQTLFLSKKELPGVLETEVTYQFIDQSFQEF	LAALSYLLEDGGV	601	650
caspase_recruitment_protein	(595)	GLDCAIISTFLKMG--LQEHPIPLSYFIHL	CQFEFFAAMSYVLEDEK-		
cryopyrin	(491)	GLQKADVSAFLRMN-LQKEVDCEKFSFIHMT	FQFEFFAAMYLLLEEKE		
Nucleotide_Binding_site	(446)	GVQESDILRLFLDGD-LLRQDRVSKGYSFIHLSFQQ	FLTALFYTLLEKEEE		
	651				700
HLRSI1	(253)	PTAAAG-----VGTLLRGDAQPHS	LVLTTTRFLFGLLSAERM		
caspase_recruitment_protein	(642)	-----GRGKHSNCIID	EKTLEAYGTHGLFGASTTRFL	GLLSDEGERE	
cryopyrin	(540)	GRTNVPGSRILKLPSRDVIVLLENYCKE	EKGYLIFVVRFLFGLVNCERTSY		
Nucleotide_Binding_site	(495)	EDRDGHTWDIG----DVQKLLSGVER	LRNPDLIQAGYVSFGLANEKRAKE		
	701				750
HLRSI1	(293)	TERHFGCMVSERVKQEA	LRWVQCQGCPCGVAPEVTEGAKGLE	EDTEEP	
caspase_recruitment_protein	(686)	MENIFHCR	LSQ--GRNLMQWVPSL-----QLLLQPHS	-----	
cryopyrin	(590)	LEKKLSCKTISQ	IRLELLKWEVK-----AKAKKLLQIQPSQ		
Nucleotide_Binding_site	(541)	LEATFGCRMSPDIKQELLRC	DISC-----KGGHSTVTDLO		

FIG. 2B-2

			751				800
			(343)	EEEEEPNYP	LELLYCLYETOEDAFVRQALCRFPETALQ	RVRF	CRMDVAV
	HLRRSI1		(716)	-----	LESLHCLYETRINKTFLTQVMHFF	ENGMC--	VEDTMELLV
	caspase_recruitment_protein		(626)	-----	LELFYCLYEMQEEDEVRAMDYFPK	IEIN--	ISTRMDHMV
	cryopyrin		(576)	-----	ELLGCLYESQEEELVKEVMAQFKEISLH	----	LNAV
	Nucleotide_Binding_site						DVVP
			801				850
			(393)	LSYCVRC	CPAGQALRLISCRLLVAAQ	EKKKKSIGKRLQASL	CGSSQ----
	HLRRSI1		(754)	CTFCIKF	SRHVKKLQLIEGRQHRSTWSP	SMVVLFRWVP	VTDAWQILFS-
	caspase_recruitment_protein		(664)	SSFCTEN	CHRVESLSLGFTHNMPKEEEEE	EKEGRHLD	MVQVLPSSSHAA
	cryopyrin		(612)	SSFQV	KHCRNTQKMSLQVTKENLP	ENVTA	SESDAEVERSQDDQHMPFWT
	Nucleotide_Binding_site						
			851				900
			(439)	-----	-----	-----	-----
	HLRRSI1		(803)	-----	-----	-----	-----
	caspase_recruitment_protein		(714)	CSHG	VN	SH	-----
	cryopyrin		(662)	DLCS	IFGS	NKDL	MGLAINDSFLSASLVRILCEQIASD
	Nucleotide_Binding_site						TCHLQ
							RVVFKNIS



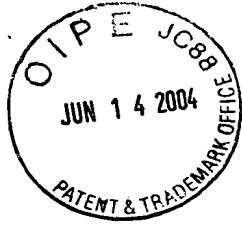
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FIG. 2B-3

HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	(439) (803) (725) (712)	901 -----GTTKQLPASLLEPLFOAMTDPPLCHLSLT -----VLKVRNLIKELDSCNSLSHSAVKSLSCKTLRPRCLLETLR SIFCRGLFSLVSTQSLELSDNSLGDPEGRVLCETLOHPGCNIRRLW PADAHRLNLCALRGCHKTVTYLTLOQNDQDDMFPA LCEVLRHPECNIRYLG 950
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	(468) (844) (775) (762)	951 LSHCKIIPDAVCPRDLSEALRAAPALTETELGILLNRLSEAGLRMLSEGLAWPQ LAGCGLTAEDCKDLAFGLRANQITLTELDSLSEFNVLM DAGAKHLCCQLRQPS LCRCGLSHECCFDISLVSSNOKLVELDLSDNALGDFGIRLLCVGLKHLL LVSCSATTOQWADLSLAEVNVQSLTCVNLSDNELDEGAKLLYTTLRHPK 1000
HLRRSI1 caspase_recruitment_protein cryopyrin Nucleotide_Binding_site	(518) (894) (825) (812)	1001 CRVQTVRQQLPDPQ-RGLQYLVGM LRQSPALTTLDLSCGLPAPMVLYLC CKLQRLQLVSCGLTSDCCQDLASVLSASPSLKELDLQNNLDVGVRLC CNLKKLWLVSCCLTSACCCDLASVLSLSTSHSLTRLVGCENALGDSGVAILC CFLQRLSLENCHLTETANCKDLAAVLVVSRELTHLCLAKNPICNTGVKFLC 1050



FIG. 2B-4

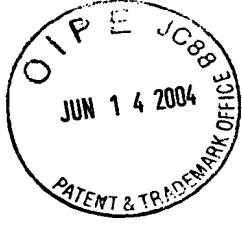


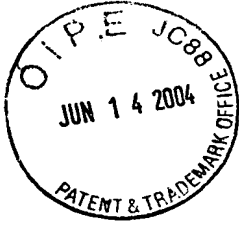
		1051			1100
HLRRSI1		(567)	AVLQHQCCGLQTLSLASVFLSEQSLQELQAVKRAKPDLVITTPALDGHPO		
caspase_recruitment_protein		(944)	EGLRHPACKLIRGLDQTLSDVMRQELRALEQEKPOLLIFSRRKPSVMT		
cryopyrin		(875)	EKAQNPQCNLQKGLVNSGLTSVCCSALSSVLSITNQNLTHLYLRGNITLGD		
Nucleotide_Binding_site		(862)	EGLRYPECKLQTLVLMNCDITSDGCCDLTKLLOEKSSLLCLDLGLNHIGV		
		1101			1150
HLRRSI1		(617)	PPKELITSTF-----		
caspase_recruitment_protein		(994)	PIEGLDTGEMSNSTSLKRRQLGSERAASHVAQANLKLDDVSKIPIAEI		
cryopyrin		(925)	KCHKLLCEGLLHPDCKLQVLELDNENLTSHCCWDLSTLLTSQSILRKLSL		
Nucleotide_Binding_site		(912)	KGMKELCEALRKPLCNLRCLWLWGCSTPPFSCEDLCSALSN-QSLVTLDL		
		1151			1200
HLRRSI1		(626)	-----		
caspase_recruitment_protein		(1044)	AEESSPEVVPVELLCVPSPAQSGDLHTKPLGTDDEFWGPTGPVATEVVDK		
cryopyrin		(975)	CNN---DLGDLGVMMFCEVLKQSSCLLQNLGLSEMVFNYETKSALETLOE		
Nucleotide_Binding_site		(961)	CQN---PLGSSGVKMLFETLTCCSSGTLRLRLKIDDFNDELNKLLEEEFE		

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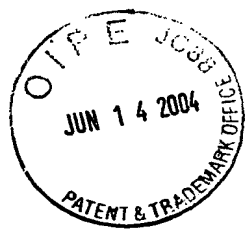
FIG. 2C-1

HLRRSI1	(626)	1201	1250
caspase_recruitment_protein	(1094)		
cryopyrin	(1022)		
Nucleotide_Binding_site	(1008)		
HLRRSI1	(626)	1251	1300
caspase_recruitment_protein	(1144)		
cryopyrin	(1035)		
Nucleotide_Binding_site	(1034)		
HLRRSI1	(626)	1301	1350
caspase_recruitment_protein	(1194)		
cryopyrin	(1035)		
Nucleotide_Binding_site	(1034)		





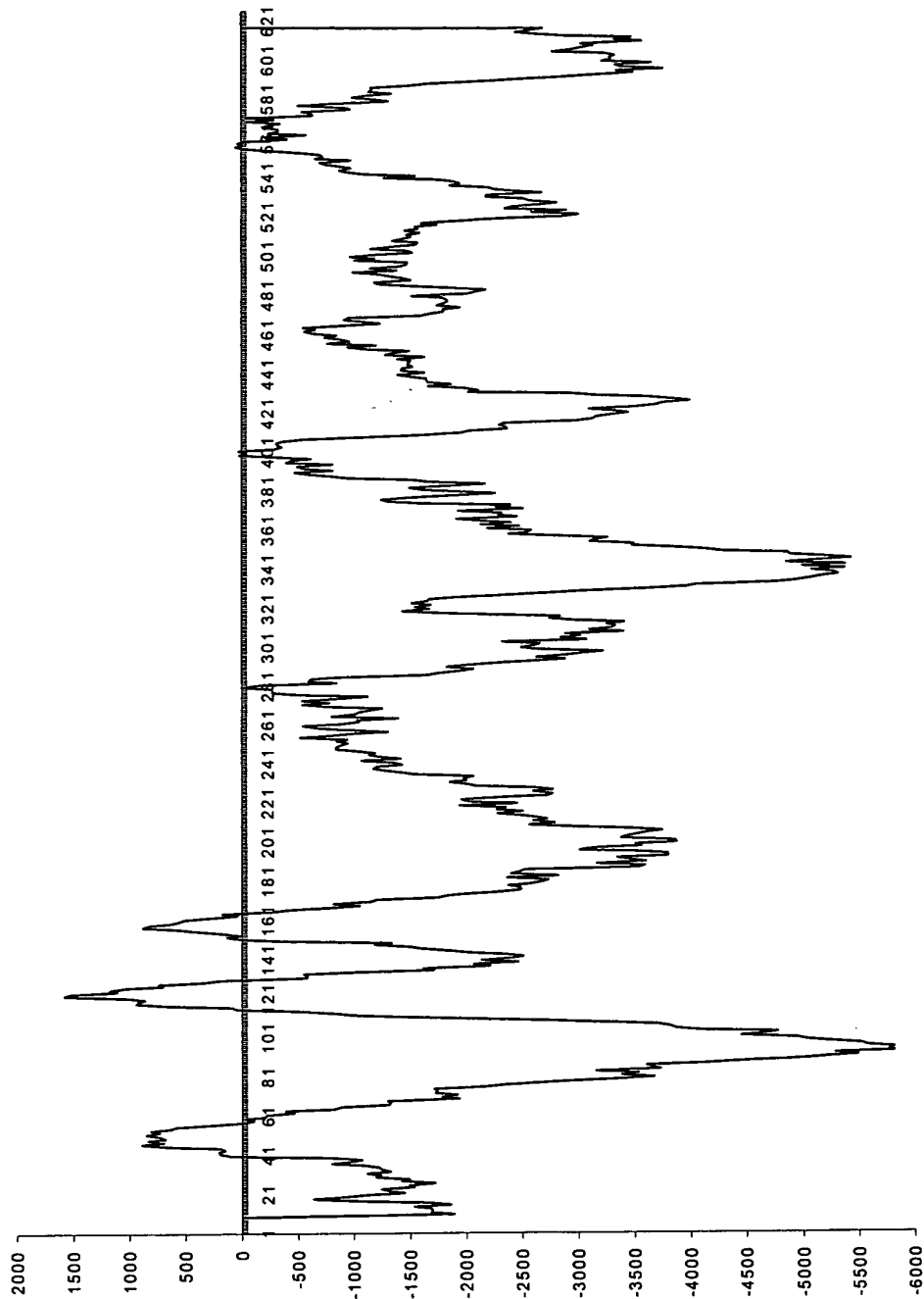
HLRRSI1	1351	1400
caspase_recruitment_protein	(626)	----
cryopyrin	(1244)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHLSGIRLQVK
Nucleotide_Binding_site	(1035)	----
	(1034)	----
HLRRSI1	1401	1450
caspase_recruitment_protein	(626)	----
cryopyrin	(1294)	DKKDETLVWEALVKPGDIMPATTLIPPACIAVPSPLDAPQLLHFVDQYRE
Nucleotide_Binding_site	(1035)	----
	(1034)	----
HLRRSI1	1451	1500
caspase_recruitment_protein	(626)	----
cryopyrin	(1344)	QLIARVTSVEVLDKLHGQVLSQEYERVLAEINTRPSQMRKLFSLSQSWD
Nucleotide_Binding_site	(1035)	----
	(1034)	----
HLRRSI1	1501	1536
caspase_recruitment_protein	(626)	----
cryopyrin	(1394)	RKCKDGLYQALKETHPHLIMELWEKSKKGLPLSS
Nucleotide_Binding_site	(1035)	----
	(1034)	----

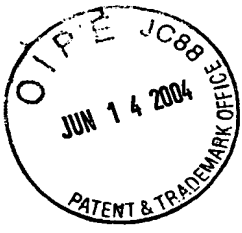


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FIG. 3

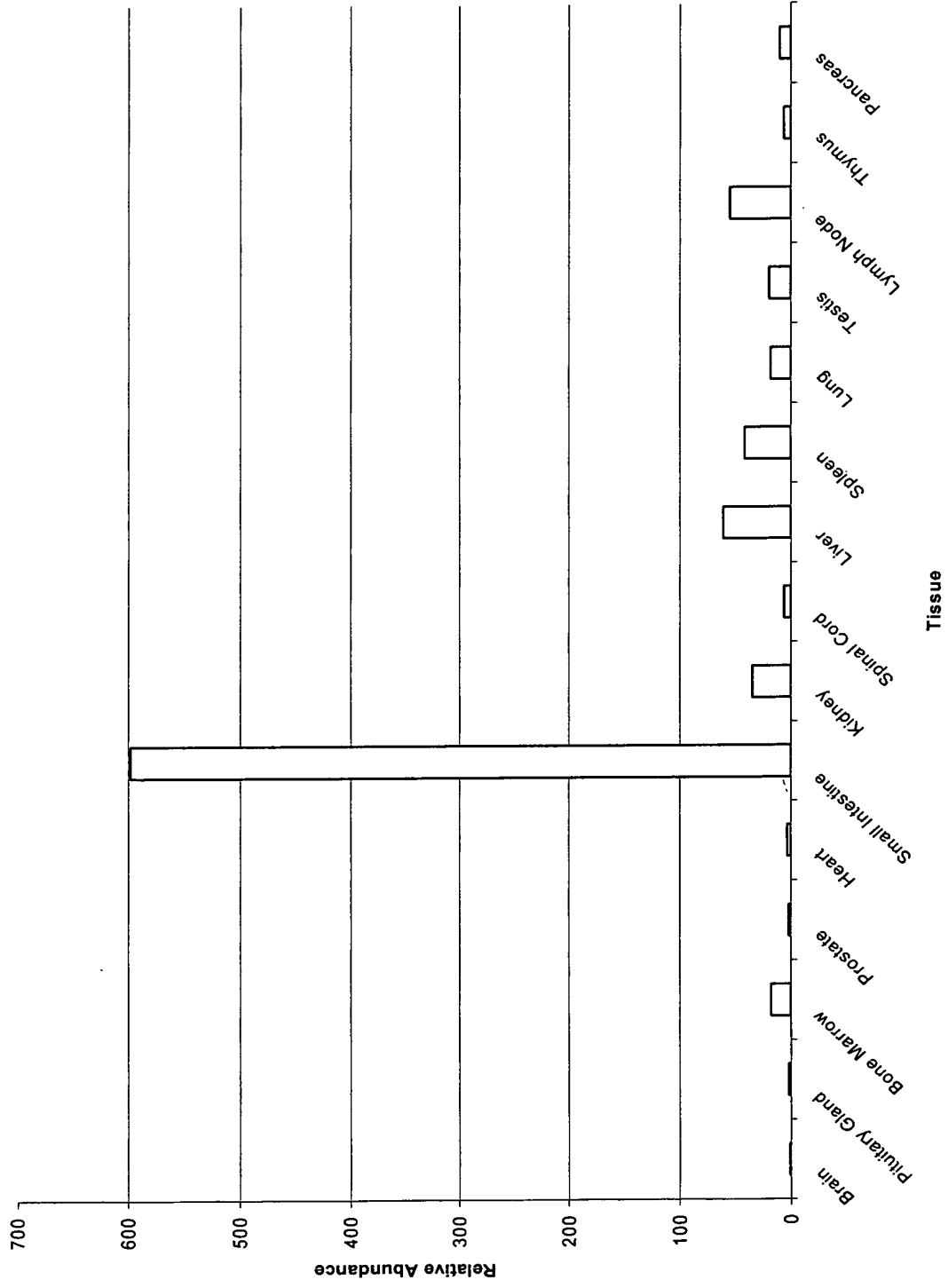


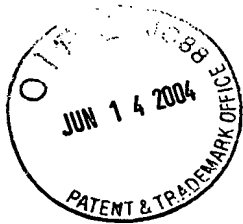


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FIG. 4





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FIG. 5

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%